IN THE CLAIMS

Amend the claims as follows.

Claims 1-42 (Canceled).

43. (Currently Amended) An *in vitro* diagnostic method for detecting a translocation of DNA sequences involved in cancer, said translocation forming at least one rearranged fusion gene, said at least one rearranged fusion gene comprising a target gene and a partner gene, said method comprising the steps of:

a) indiscriminately reverse transcribing RNA extracted from a patient sample with a first primer, said first primer being a random anchored primer, said reverse transcribing producing patient cDNA, said anchored primer comprising a unique 5' portion and a 3' random portion,

b) amplifying all of the patient cDNA with a first pair of primers, said first pair of primers comprising a second primer and a third primer, said second primer being complementary to and binding specifically with cDNA of said target gene and said third primer being complementary to and binding specifically with a first part of the unique 5' portion of said anchored primer, said amplifying all of the patient cDNA producing a first collection of amplified products containing a first 5' target gene portion and a first 3' anchor portion,

c) amplifying said collection of amplified products with a second pair of primers in a nested amplification reaction, said second set of primers comprising a fourth primer and a fifth primer, said fourth primer being complementary to and binding specifically

with said target gene at a position 3' to said second primer, said fifth primer containing a sequence which binds to at least a portion of said first part of the unique 5' portion of said anchored primer, said amplifying said collection producing a second collection of amplified products containing a second 5' target gene portion and a second 3' anchor portion, said second collection of amplified products further comprising detectably labeled nucleotides incorporated in to said products during amplification,

d) contacting said second collection of amplified products with at least one nucleic acid probe or at least one plurality of nucleic acid probes, wherein said at least one nucleic acid probe or each of said plurality of nucleic acid probes is specific for a partner gene, under conditions wherein any cDNA corresponding to said partner gene of the fusion gene present in said collection will hybridize with said probe, and

e) detecting any detectably labeled cDNA from said second collection of amplified products bound to said probe as an indication of translocation of DNA sequences.

44. (Previously Presented) The method of claim 43, wherein any one of the first primer, the second primer, the third primer, the fourth primer and the fifth primer is 25 to 40 nucleotides in length.

45. (Previously Presented) The method of claim 43, wherein said detectably labeled nucleotides are nucleotides bound directly or indirectly to a marker selected from the group consisting of digoxigenine, biotin and a fluorophore.

46. (Previously Presented) The method of claim 43, wherein said probes are covalently bound to a solid surface.

47. (Previously Presented) The method of claim 46, wherein said solid surface is selected from the group consisting of an ELISA plate and a DNA chip.

48. (Previously Presented) The method of claim 43, wherein said first primer consists of a sequence containing a cassette of 40 to 60 nucleotides, wherein said 3' random portion comprises a sequence of 10 to 20 (dT)s or a sequence of a random nucleotide pattern.

49. (Previously Presented) The method of claim 43, wherein the target gene is a MLL gene.

50. (Previously Presented) The method of claim 49 wherein said probes are specific for known MLL fusion partner genes.

51. (Previously Presented) The method of claim 50, wherein said detectably labeled nucleotides are nucleotides bound directly or indirectly to a marker selected from the group consisting of digoxigenine, biotin and a fluorophore.

52. (Currently Amended) The method of claim 51, wherein the probes are bound to a ~~said~~ solid surface ~~is~~ selected from the group consisting of an ELISA plate and a DNA chip.

53. (Previously Presented) The method of claim 52 wherein said marker is digoxygenine, said detecting comprises contacting said marker with anti-digoxygenine antibodies coupled to an enzyme, said enzyme being capable of reacting with a substrate of said enzyme to release a detectable product.

54. (Previously Presented) The method of claim 49, wherein said cancer is leukemia.

55. (Previously Presented) The method of claim 54, wherein said cancer is a solid tumor.

56. (Previously Presented) The method of claim 55, wherein said cancer is a Ewing tumor.

57. (Previously Presented) The method of claim 43 wherein step (e) further comprises identifying said partner gene of the fusion gene from binding of said probes.

Claim 58. (Canceled)

59. (Currently Amended) The kit according to claim 61~~claim 58~~, wherein said at least one probe is bound to the solid support through a biotin group bonded to streptavidin coupled to said support.

Claim 60. (Canceled)

61. (Currently Amended) A kit for an *in vitro* diagnostic method for detecting translocation of DNA sequences involved in cancer, said translocation forming at least one rearranged fusion gene, said rearranged fusion gene comprising a target gene and a partner gene, said kit comprising a pair of primers, said pair of primers comprising a first primer and a second primer, said first primer being complementary to and binding specifically with cDNA of said target gene and said second primer being complementary to and binding specifically with a first part of a unique 5' portion of an anchored primer used to reverse transcribe said cDNA from mRNA transcribed from said fusion gene, said kit further comprising at least one probe specific for cDNA encoded by said partner gene, said at least one probe being bound to a ~~The kit according to claim 58 wherein the support is a~~ DNA chip solid support.

62. (Currently Amended) The kit according to claim 61~~claim 58~~ wherein the target gene is the MLL gene.